

GAP of: 0964DP54725 check: 3361 from: 1 to: 363

WPDEF Case 0964D Rad23 SwissProt P54725 Human Rad23A

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P54725. UV excision repai. . .[gi:1709983] BLink, Domains, Links

LOCUS P54725 363 aa linear PRI 15-
SEP-2003

DEFINITION UV excision repair protein RAD23 homolog A (HHR23A).

ACCESSION P54725 . . .

to: 0964sid2 check: 7022 from: 1 to: 405

WPDEF Case 0964 Rad23 SEQ ID NO: 2 corn

Case 0964 Rad23 SEQ ID NO: 2 corn

Symbol comparison table: blosum62.cmp CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl.
Acad.

Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.778
Length Weight: 2 Average Mismatch: -2.248

Quality: 503 Length: 415
Ratio: 1.386 Gaps: 11
Percent Similarity: 48.725 Percent Identity: 38.244

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

0964DP54725 x 0964sid2 October 28, 2003 11:25 ..

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      .
1 mavtitlktlqqqtfkirmepdetvkvakeieaekgrdafpvaggkliy 50
      . : .||| . |. | | . | . | | | . : | |||
1 ..MKLNVKTLKGTNFEIEASPDASVADV KRIETTQQQSTYRADQQMLIY 48
      .
51 agkilsddvpirdyrideknfvvmvmtkagqgtsappeasptaapess 100
      |||| |: : : | .|. |:|. | | | | . . . | .
49 QGKILKDETTLESNGVAENSFLVIMLSKAKASSSGASTATTAKAPATLAQ 98
      .
101 tsfpapptsgmshpppaaredkspseesapttspesv.sgsvpssgssgr 149
      . | || . . . | | . . | . | . |: . . | . .
99 PAAPVAPAASVARTPTQA..PVATAETAPPSVQPQAAPAAATVAATDDADV 146
      .
150 eedaastlvtgseyetmlteimsmg...yerervvaalrasynnphrave 196
      ||| || |. | : : |: || :||: || ||||. |||| |:::
147 YSQAASNLVFGNNLEQTIQQILDMGGGTWERDTVVRALRAAYNNPERAID 196
      .
197 ylltgipgspe.....pehgs.....vgesqvseqp 222
      || .||| . | | | | | | | | | | | | | | | |
197 YLYSGIPENVEAQPVARAPAAGQQTNQQAASPAQPAVALPVQPSPASAGP 246
      .
      .
      .
      .

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223ateaagenp.....leflrdqpqfqnmrqviqqnp 252
 . | || |: || ||| : |.: | ||
 247 NANPLNLFPQGVPSGGSNPGVVPGAGSGALDALRQLPQFQALLQLVQANP 296
 . . .
 253 allpallqqlgqenpqllqqisrhqeqfiqmlneppgeladisvegevg 302
 :| :||:| |:| |:|. | .| |:|:|. || | | .: |:.
 297 QILQPMLQELGKQNPQILRLIQENQAEFLRLVNESP.EGGPGGNILGQLA 345
 .
 303 aigeeapqmnyiqvtpqekeaiierlkalgfpeslviqayfaceknenlaa 352
 | || : |||:| |:| |:|. :|| ||: :||| |. | | |
 346 A...AVPQT...LTVTPPEEREAIQRLEGMGFNRELVLEVFFACNKDEELTA 390
 .
 353 nfl1..sqnfdde.. 363
 |:| | |:|
 391 NYLLDHGHEFDDQQQ 405